December 5, 1997, which claims priority to U.S. Provisional Application Serial No. 60/033,251, filed December 6, 1996.

Please change the paragraph beginning at Page 6, Line 8 to the following:

Figure 1 shows the nucleotide sequence of *speC* (SEQ ID NO: 1). Numbering is in reference to the ATG start codon. Possible promoter (-10, -35) and Shine-Dalgarno (SD) sequences are noted. The deduced amino acid sequence (SEQ ID NO: 2) is given below the nucleotide sequence. An asterisk after residue 27 indicates the cleavage site between the signal peptide and mature protein. Overlined nucleotides 3' of the translation stop codon are palindromic sequences.

Please change the paragraph beginning at Page 7, Line 29 to the following:

Wild type SPE-C toxin is encoded by a gene speC. The wild type SPE-C toxin has a molecular weight of 24,000 Daltons as determined by SDS PAGE of purified protein. A DNA sequence (SEQ ID NO: 1) encoding a wild type SPE-C toxin and the predicted amino acid sequence (SEQ ID NO: 2) for a wild type SPE-C toxin is shown in Figure 1. A DNA sequence encoding a wild type SPE-A toxin has been cloned in E. coli and S. aureus. Amino acid number designations in this application are made by reference to the sequence of Figure 1 with aspartate at position 28 designated as the first amino acid. The first 27 amino acids represent a leader sequence not present in the mature protein.

Please change the paragraph beginning at Page 8, Line 15 to the following:

As used herein, the definition of a wild type SPE-C toxin includes variants, such as allelic variants, of a wild type SPE-C toxin that have the same biological activity of wild type SPE-C toxin. These SPE-C toxins may have a different amino acid or their genes may have a different nucleotide sequence from that shown in Figure 1 but do not have different biological activities. Changes in amino acid sequence are phenotypically silent. Preferably, these toxin molecules have systemic lethality and enhance endotoxin shock to the same degree as wild type SPE-C

toxin shown in Figure 1. Preferably these toxins have at least 60-99% homology with wild type SPE-C toxin amino acid sequence (SEQ ID NO: 2) as shown in Figure 1 as determined using the SS2 Alignment Algorithm as described by Altschul,S. F., Bull. Math. Bio. 48:603 (1986). Proteins that have these characteristics substantially correspond to a wild type SPE C.

Please change the paragraph beginning at Page 9, Line 24 to the following:

Changes in the amino acid sequence at a particular site can be randomly made or specific changes can be selected. Once a specific site is selected it is referred to by its amino acid number designation and by the amino acid found at that site in the wild type SPE-C (SEQ ID NO: 2) as shown in Figure 1. The amino acid number designations made in this application are by reference to the sequence in Figure 1 with the aspartate at position 28 being counted as the first amino acid. Equivalent amino acids corresponding to those identified at a particular site in proteins substantially corresponding to a wild type SPE-C toxin may have different amino acid numbers depending on the reference sequence or if they are fragments. Equivalent residues are also those found in homologous molecules that can be identified as equivalent to amino acids in proteins substantially corresponding to a wild type SPE-C toxin either by comparison of primary amino acid structure or by comparison to a modeled structure as shown in Figure 1 or by comparison to a known crystal structure of a homologous molecule. It is intended that the invention cover changes to equivalent amino acids at the same or similar locations regardless of their amino acid number designation.

Please change the paragraph beginning at Page 28, Line 9 to the following:

A mutant DNA sequence encoding a mutant SPE-C toxin that has at least one change in amino acid sequence can be formed by a variety of methods depending on the type of change selected. A DNA sequence encoding a protein substantially corresponding to wild type SPE-C toxin functions as template DNA used to generate DNA sequences encoding mutant SPE-C toxins. A DNA sequence encoding wild type SPE-C toxin is shown in Figure 1 (SEQ ID NO: 1).